

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/824,834  
Source: IFWO  
Date Processed by STIC: 10/29/04

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 10/29/2004

PATENT APPLICATION: US/10/824,834

TIME: 17:07:06

Input Set : A:\HTS0130USSEQ.txt

Output Set: N:\CRF4\10292004\J824834.raw

```

3 <110> APPLICANT: Ian Popoff
4     Susan M. Freier
5     Kenneth W. Dobie
7 <120> TITLE OF INVENTION: MODULATION OF SOCS-3 EXPRESSION
9 <130> FILE REFERENCE: HTS-0130US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/824,834
C--> 11 <141> CURRENT FILING DATE: 2004-04-14
11 <150> PRIOR APPLICATION NUMBER: 60/464,212
12 <151> PRIOR FILING DATE: 2004-04-18
14 <160> NUMBER OF SEQ ID NOS: 167
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 20
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
24 <223> OTHER INFORMATION: Antisense Oligonucleotide
26 <400> SEQUENCE: 1
27 tccgtcatcg ctctcaggg                                20
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 20
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
37 <223> OTHER INFORMATION: Antisense Oligonucleotide
39 <400> SEQUENCE: 2
40 gtgcgcgcga gcccgaatc                                20
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 20
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
50 <223> OTHER INFORMATION: Antisense Oligonucleotide
52 <400> SEQUENCE: 3
53 atgcattctg cccccaagga                                20
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 850
58 <212> TYPE: DNA
59 <213> ORGANISM: H. sapiens
61 <220> FEATURE:
63 <220> FEATURE:
64 <221> NAME/KEY: CDS
65 <222> LOCATION: (107)...(784)
67 <400> SEQUENCE: 4

```

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```

68 gcgccttcct ctccgcagcc ccccgggatg cggtagcggc cgctgtgcgg aggccgcgaa      60
70 gcagctgcag ccgcgcgcgc gcagatccac gctggctccg tgcgcc atg gtc acc      115
71                                     Met Val Thr
72                                     1
74 cac agc aag ttt ccc gcc gcc ggg atg agc cgc ccc ctg gac acc agc      163
75 His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu Asp Thr Ser
76      5      10      15
78 ctg cgc ctc aag acc ttc agc tcc aag agc gag tac cag ctg gtg gtg      211
79 Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln Leu Val Val
80 20      25      30      35
82 aac gca gtg cgc aag ctg cag gag agc ggc ttc tac tgg agc gca gtg      259
83 Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp Ser Ala Val
84      40      45      50
86 acc ggc ggc gag gcg aac ctg ctg ctc agt gcc gag ccc gcc ggc acc      307
87 Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro Ala Gly Thr
88      55      60      65
90 ttt ctg atc cgc gac agc tcg gac cag cgc cac ttc ttc gcg ctc agc      355
91 Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe Ala Leu Ser
92      70      75      80
94 gtc aag acc cag tct ggg acc aag aac ctg cgc atc cag tgt gag ggg      403
95 Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln Cys Glu Gly
96      85      90      95
98 ggc agc ttc tct ctg cag agc gat ccc cgg agc acg cag ccc gtg ccc      451
99 Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln Pro Val Pro
100 100      105      110      115
102 cgc ttc gac tgc gtg ctc aag ctg gtg tac cac tac atg ccg ccc cct      499
103 Arg Phe Asp Cys Val Leu Lys Leu Val Tyr His Tyr Met Pro Pro Pro
104      120      125      130
106 gga gcc ccc tcc ttc ccc tcg cca cct act gaa ccc tcc tcc gag gtg      547
107 Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser Ser Glu Val
108      135      140      145
110 ccc gag cag ccg tct gcc cag cca ctc cct ggg agt ccc ccc aga aga      595
111 Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro Pro Arg Arg
112      150      155      160
114 gcc tat tac atc tac tcc ggg ggc gag aag atc ccc ctg gtg ttg agc      643
115 Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu Val Leu Ser
116      165      170      175
118 cgg ccc ctc tcc tcc aac gtg gcc act ctt cag cat ctc tgt cgg aag      691
119 Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu Cys Arg Lys
120 180      185      190      195
122 acc gtc aac ggc cac ctg gac tcc tat gag aaa gtc acc cag ctg ccg      739
123 Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr Gln Leu Pro
124      200      205      210
126 ggg ccc att cgg gag ttc ctg gac cag tac gat gcc ccg ctt taa      784
128 ggggtaaaagg gcgcaaaggg catgggtcgg gagagggggac gcaggccoct ctctccgtg      844
130 gcacat      850
133 <210> SEQ ID NO: 5
134 <211> LENGTH: 19
135 <212> TYPE: DNA

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```

136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
140 <223> OTHER INFORMATION: PCR Primer
142 <400> SEQUENCE: 5
143 ggaccagcgc cacttcttc
146 <210> SEQ ID NO: 6
147 <211> LENGTH: 20
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
153 <223> OTHER INFORMATION: PCR Primer
155 <400> SEQUENCE: 6
156 actggatgcg caggttcttg
160 <210> SEQ ID NO: 7
161 <211> LENGTH: 25
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
167 <223> OTHER INFORMATION: PCR Probe
169 <400> SEQUENCE: 7
170 ctcagcgtca agaccagtc tggga
173 <210> SEQ ID NO: 8
174 <211> LENGTH: 19
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
180 <223> OTHER INFORMATION: PCR Primer
182 <400> SEQUENCE: 8
183 gaaggtgaag gtcggagtc
186 <210> SEQ ID NO: 9
187 <211> LENGTH: 20
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
193 <223> OTHER INFORMATION: PCR Primer
195 <400> SEQUENCE: 9
196 gaagatggtg atgggatttc
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 20
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
206 <223> OTHER INFORMATION: PCR Probe
208 <400> SEQUENCE: 10
209 caagcttccc gttctcagcc
212 <210> SEQ ID NO: 11
213 <211> LENGTH: 2187
214 <212> TYPE: DNA
215 <213> ORGANISM: M. musculus

```

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```

217 <220> FEATURE:
219 <220> FEATURE:
220 <221> NAME/KEY: CDS
221 <222> LOCATION: (18)...(695)
223 <400> SEQUENCE: 11
224 cgctggctcc gtgcgcc atg gtc acc cac agc aag ttt ccc gcc gcc ggg 50
225             Met Val Thr His Ser Lys Phe Pro Ala Ala Gly
226             1             5             10
228 atg agc cgc ccc ctg gac acc agc ctg cgc ctc aag acc ttc agc tcc 98
229 Met Ser Arg Pro Leu Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser
230             15             20             25
232 aaa agc gag tac cag ctg gtg gtg aac gcc gtg cgc aag ctg cag gag 146
233 Lys Ser Glu Tyr Gln Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu
234             30             35             40
236 agc gga ttc tac tgg agc gcc gtg acc ggc ggc gag gcg aac ctg ctg 194
237 Ser Gly Phe Tyr Trp Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu
238             45             50             55
240 ctc agc gcc gag ccc gcg ggc acc ttt ctt atc cgc gac agc tcg gac 242
241 Leu Ser Ala Glu Pro Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp
242             60             65             70             75
244 cag cgc cac ttc ttc acg ttg agc gtc aag acc cag tcg ggg acc aag 290
245 Gln Arg His Phe Phe Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys
246             80             85             90
248 aac cta cgc atc cag tgt gag ggg ggc agc ttt tcg ctg cag agt gac 338
249 Asn Leu Arg Ile Gln Cys Glu Gly Ser Phe Ser Leu Gln Ser Asp
250             95             100             105
252 ccc cga agc acg cag cca gtt ccc cgc ttc gac tgt gta ctc aag ctg 386
253 Pro Arg Ser Thr Gln Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu
254             110             115             120
256 gtg cac cac tac atg ccg cct cca ggg acc ccc tcc ttt tct ttg cca 434
257 Val His His Tyr Met Pro Pro Pro Gly Thr Pro Ser Phe Ser Leu Pro
258             125             130             135
260 ccc acg gaa ccc tcg tcc gaa gtt ccg gag cag cca cct gcc cag gca 482
261 Pro Thr Glu Pro Ser Ser Glu Val Pro Glu Gln Pro Pro Ala Gln Ala
262             140             145             150             155
264 ctc ccc ggg agt acc ccc aag aga gct tac tac atc tat tct ggg ggc 530
265 Leu Pro Gly Ser Thr Pro Lys Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly
266             160             165             170
268 gag aag att ccg ctg gta ctg agc cga cct ctc tcc tcc aac gtg gcc 578
269 Glu Lys Ile Pro Leu Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala
270             175             180             185
272 acc ctc cag cat ctt tgt cgg aag act gtc aac ggc cac ctg gac tcc 626
273 Thr Leu Gln His Leu Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser
274             190             195             200
276 tat gag aaa gtg acc cag ctg cct gga ccc att cgg gag ttc ctg gat 674
277 Tyr Glu Lys Val Thr Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp
278             205             210             215
280 cag tat gat gct cca ctt taa ggagcaaaag gggtcagaggg gggcctgggt 725
281 Gln Tyr Asp Ala Pro Leu *

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```

282 220                               225
284 cggtcggtcg cctctcctcc gaggcacatg gcacaagcac aaaaatccag ccccaacggt 785
286 cggtagctcc cagttagcca ggggcagatt ggcttcttcc tcaggccctc cactcccgca 845
288 gagtagagct ggcaggacct ggaattcgct tgaggggagg gggagctgcc acctgctttc 905
290 cccctcccc cagctccagc ttctttcaag tggagccagc cggcctggcc tgggtgggaca 965
292 atacctttga caagcggact ctccccctcc cttcctccac acccctctg cttcccaagg 1025
294 gaggtgggga cacctccaag tgttgaactt agaactgcaa ggggaatctt caaactttcc 1085
296 cgctggaact tgtttgcgct ttgatttggt ttgatcaaga gcaggcacct gggggaagga 1145
298 tggaagagaa aaggggtgtg gaaggggttt tatgctggcc aaagaaataa ccactcccac 1205
300 tgcccaacct aggtgaggag tgggtggctcc tggctctggg gagagtggca aggggtgacc 1265
302 tgaagagagc tatactggtg ccaggctcct ctccatgggg cagctaataa aacctcgcag 1325
304 atcccttgca cccagaacc ctccccgttg tgaagaggca gtagcattta gaaggagac 1385
306 agatgaggct ggtgagctgg ccgccttttc caacaccgaa gggaggcaga tcaacagatg 1445
308 agccatcttg gagcccaggt ttccccgtga gcagatggag ggttctgctt tgtctctcct 1505
310 atgtggggct aggagactcg ccttaaatac cctctgtccc agggatgggg attggcacac 1565
312 aaggagccaa acacagccaa taggcagaga gttgagggat tcaccaggt ggctacaggc 1625
314 caggggaagt ggctgcaggg gagagacca gtcactccag gagactcctg agttaacact 1685
316 gggaagacat tggccagtc tagtcatctc tcggtcagta ggtccgagag cttccaggcc 1745
318 ctgcacagcc ctctttctc acctgggggg aggcaggagg tgatggagaa gccttcccat 1805
320 gccgctcaca ggggcctcac ggggaatgcag cagccatgca attacctgga actggtcctg 1865
322 tggtggggag aaacaagttt tctgaagtca ggtatggggc tgggtggggc agctgtgtgt 1925
324 tggggtggct tttttctctc tgttttgaat aatgtttaca atttgctca atcactttta 1985
326 taaaaatcca cctccagccc gccctctcc ccactcaggc ctcgagget gtctgaagat 2045
328 gcttgaaaaa ctcaaccaa tcccagttca actcagactt tgcacatata tttatatatta 2105
330 tactcagaaa agaaacattt cagtaattta taataaaaga gcactatttt ttaatgaaaa 2165
332 aaaaaaaaaa aaaaaaaaaa aa                                     2187
336 <210> SEQ ID NO: 12
337 <211> LENGTH: 22
338 <212> TYPE: DNA
339 <213> ORGANISM: Artificial Sequence
341 <220> FEATURE:
343 <223> OTHER INFORMATION: PCR Primer
345 <400> SEQUENCE: 12
346 ccttcagctc caaaagcgag ta                                     22
349 <210> SEQ ID NO: 13
350 <211> LENGTH: 18
351 <212> TYPE: DNA
352 <213> ORGANISM: Artificial Sequence
354 <220> FEATURE:
356 <223> OTHER INFORMATION: PCR Primer
358 <400> SEQUENCE: 13
359 ggtcacggcg ctccagta                                     18
362 <210> SEQ ID NO: 14
363 <211> LENGTH: 20
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial Sequence
367 <220> FEATURE:
369 <223> OTHER INFORMATION: PCR Probe
371 <400> SEQUENCE: 14

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/824,834

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Input Set : A:\HTS0130USSEQ.txt

Output Set: N:\CRF4\10292004\J824834.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date